



## SEQUENCE LISTING

<110> SHERMAN, LINDA A.  
LUSTGARTEN, JOSEPH

<120> RECOMBINANT CONSTRUCTS ENCODING T CELL RECEPTORS  
SPECIFIC FOR HUMAN HLA-RESTRICTED TUMOR ANTIGENS

<130> 48340/55793-DIV

<140> 09/774,681

<141> 2001-02-01

<150> 08/812,393

<151> 1997-03-05

<150> 60/012,845

<151> 1996-03-05

<160> 64

<170> PatentIn Ver. 2.1

<210> 1

<211> 1350

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)..(1332)

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<223> Description of Artificial Sequence: Synthetic  
single chain TCR derivative nucleotide sequence

<400> 1

ctc	gag	atg	cag	agg	aac	ctg	gga	gct	gtg	ctg	ggg	att	ctg	tgg	gtg	48
Leu	Glu	Met	Gln	Arg	Asn	Leu	Gly	Ala	Val	Leu	Gly	Ile	Leu	Trp	Val	
1				5					10					15		
cag	att	tgc	tgg	ctg	aaa	gaa	cag	caa	gtg	cag	cag	agt	ccc	gca	tcc	96
Gln	Ile	Cys	Trp	Leu	Lys	Glu	Gln	Gln	Val	Gln	Gln	Ser	Pro	Ala	Ser	
			20					25					30			
ttg	gtt	ctg	cag	gag	ggg	gag	aac	gca	gag	ctc	cag	tgt	agc	ttt	tcc	144
Leu	Val	Leu	Gln	Glu	Gly	Glu	Asn	Ala	Glu	Leu	Gln	Cys	Ser	Phe	Ser	
		35				40						45				
atc	ttt	aca	aac	cag	gtg	cag	tgg	ttt	tac	caa	cgt	cct	ggg	gga	aga	192
Ile	Phe	Thr	Asn	Gln	Val	Gln	Trp	Phe	Tyr	Gln	Arg	Pro	Gly	Gly	Arg	
		50				55					60					
ctc	gtc	agc	ctg	ttg	tac	aat	cct	tct	ggg	aca	aag	cag	agt	ggg	aga	240
Leu	Val	Ser	Leu	Leu	Tyr	Asn	Pro	Ser	Gly	Thr	Lys	Gln	Ser	Gly	Arg	
		65			70					75					80	

ctg aca tcc aca aca gtc att aaa gaa cgt cgc agc tct ttg cac att	288
Leu Thr Ser Thr Thr Val Ile Lys Glu Arg Arg Ser Ser Leu His Ile	
85 90 95	
tcc tcc tcc cag atc aca gac tca ggc act tat ctc tgt gcc tca aat	336
Ser Ser Ser Gln Ile Thr Asp Ser Gly Thr Tyr Leu Cys Ala Ser Asn	
100 105 110	
tct gga gga agc aat gca aag cta acc ttc ggg aaa ggc act aaa ctc	384
Ser Gly Gly Ser Asn Ala Lys Leu Thr Phe Gly Lys Gly Thr Lys Leu	
115 120 125	
tct gtt aaa tca ggt ggc gga ggg tct ggc ggg ggt gga tcc ggg ggt	432
Ser Val Lys Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly	
130 135 140	
gga ggc tca gag gct gca gtc acc caa agc cca aga aac aag gtg gca	480
Gly Gly Ser Glu Ala Ala Val Thr Gln Ser Pro Arg Asn Lys Val Ala	
145 150 155 160	
gta aca gga gga aag gtg aca ttg agc tgt aat cag act aat aac cac	528
Val Thr Gly Gly Lys Val Thr Leu Ser Cys Asn Gln Thr Asn Asn His	
165 170 175	
aac aac atg tac tgg tat cgg cag gac acg ggg cat ggg ctg agg ctg	576
Asn Asn Met Tyr Trp Tyr Arg Gln Asp Thr Gly His Gly Leu Arg Leu	
180 185 190	
atc cat tat tca tat ggt gct ggc agc act gag aaa gga gat atc cct	624
Ile His Tyr Ser Tyr Gly Ala Gly Ser Thr Glu Lys Gly Asp Ile Pro	
195 200 205	
gat gga tac aag gcc tcc aga cca agc caa gag aac ttc tcc ctc att	672
Asp Gly Tyr Lys Ala Ser Arg Pro Ser Gln Glu Asn Phe Ser Leu Ile	
210 215 220	
ctg gag ttg gct acc ccc tct cag aca tca gtg tac ttc tgt gcc agc	720
Leu Glu Leu Ala Thr Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser	
225 230 235 240	
ggt gag aca ggg acc aac gaa aga tta ttt ttc ggt cat gga acc aag	768
Gly Glu Thr Gly Thr Asn Glu Arg Leu Phe Phe Gly His Gly Thr Lys	
245 250 255	
ctg tct gtc ctg act agt aac tcc atc atg tac ttc agc cac ttc gtg	816
Leu Ser Val Leu Thr Ser Asn Ser Ile Met Tyr Phe Ser His Phe Val	
260 265 270	
ccg gtc ttc ctg cca gcg aag ccc acc acg acg cca gcg ccg cga cca	864
Pro Val Phe Leu Pro Ala Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro	
275 280 285	
cca aca ccg gcg ccc acc atc gcg tcg cag ccc ctg tcc ctg cgc cca	912
Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro	
290 295 300	

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tct agt tct aga gat ccc aaa ctc tgc tac ctg ctg gat gga atc ctc 960
Ser Ser Ser Arg Asp Pro Lys Leu Cys Tyr Leu Leu Asp Gly Ile Leu
305 310 315 320

ttc atc tat ggt gtc att ctc act gcc ttg ttc ctg aga gtg aag ttc 1008
Phe Ile Tyr Gly Val Ile Leu Thr Ala Leu Phe Leu Arg Val Lys Phe
325 330 335

agc agg agc gca gac gcc ccc gcg tac cag cag ggc cag aac cag ctc 1056
Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu
340 345 350

tat aac gag ctc aat cta gga cga aga gag gag tac gat gtt ttg gac 1104
Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp
355 360 365

aag aga cgt ggc cgg gac cct gag atg ggg gga aag ccg aga agg aag 1152
Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys
370 375 380

aac cct cag gaa ggc ctg tac aat gaa ctg cag aaa gat aag atg gcg 1200
Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala
385 390 395 400

gag gcc tac agt gag att ggg atg aaa ggc gag cgc cgg agg ggc aag 1248
Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
405 410 415

ggg cac gat ggc ctt tac cag ggt ctc agt aca gcc acc aag gac acc 1296
Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
420 425 430

tac gac gcc ctt cac atg cag gcc ctg ccc cct cgc taa gcg gcc gcc 1344
Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
435 440

acc gcg 1350

<210> 2
<211> 444
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
single chain TCR protein

<400> 2
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Gln Ile Cys Trp Leu Lys Glu Gln Gln Val Gln Gln Ser Pro Ala Ser
20 25 30

Leu Val Leu Gln Glu Gly Glu Asn Ala Glu Leu Gln Cys Ser Phe Ser
35 40 45

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Ile	Phe	Thr	Asn	Gln	Val	Gln	Trp	Phe	Tyr	Gln	Arg	Pro	Gly	Gly	Arg		
50						55					60						
Leu	Val	Ser	Leu	Leu	Tyr	Asn	Pro	Ser	Gly	Thr	Lys	Gln	Ser	Gly	Arg		
65					70					75					80		
Leu	Thr	Ser	Thr	Thr	Val	Ile	Lys	Glu	Arg	Arg	Ser	Ser	Leu	His	Ile		
				85					90					95			
Ser	Ser	Ser	Gln	Ile	Thr	Asp	Ser	Gly	Thr	Tyr	Leu	Cys	Ala	Ser	Asn		
			100					105					110				
Ser	Gly	Gly	Ser	Asn	Ala	Lys	Leu	Thr	Phe	Gly	Lys	Gly	Thr	Lys	Leu		
		115					120					125					
Ser	Val	Lys	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly		
	130					135					140						
Gly	Gly	Ser	Glu	Ala	Ala	Val	Thr	Gln	Ser	Pro	Arg	Asn	Lys	Val	Ala		
145					150					155					160		
Val	Thr	Gly	Gly	Lys	Val	Thr	Leu	Ser	Cys	Asn	Gln	Thr	Asn	Asn	His		
				165					170					175			
Asn	Asn	Met	Tyr	Trp	Tyr	Arg	Gln	Asp	Thr	Gly	His	Gly	Leu	Arg	Leu		
		180						185					190				
Ile	His	Tyr	Ser	Tyr	Gly	Ala	Gly	Ser	Thr	Glu	Lys	Gly	Asp	Ile	Pro		
		195					200					205					
Asp	Gly	Tyr	Lys	Ala	Ser	Arg	Pro	Ser	Gln	Glu	Asn	Phe	Ser	Leu	Ile		
	210					215					220						
Leu	Glu	Leu	Ala	Thr	Pro	Ser	Gln	Thr	Ser	Val	Tyr	Phe	Cys	Ala	Ser		
225					230					235					240		
Gly	Glu	Thr	Gly	Thr	Asn	Glu	Arg	Leu	Phe	Phe	Gly	His	Gly	Thr	Lys		
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Leu	Ser	Val	Leu	Thr	Ser	Asn	Ser	Ile	Met	Tyr	Phe	Ser	His	Phe	Val		
		260						265					270				
Pro	Val	Phe	Leu	Pro	Ala	Lys	Pro	Thr	Thr	Thr	Pro	Ala	Pro	Arg	Pro		
		275					280					285					
Pro	Thr	Pro	Ala	Pro	Thr	Ile	Ala	Ser	Gln	Pro	Leu	Ser	Leu	Arg	Pro		
	290					295					300						
Ser	Ser	Ser	Arg	Asp	Pro	Lys	Leu	Cys	Tyr	Leu	Leu	Asp	Gly	Ile	Leu		
305					310					315					320		
Phe	Ile	Tyr	Gly	Val	Ile	Leu	Thr	Ala	Leu	Phe	Leu	Arg	Val	Lys	Phe		
				325					330					335			
Ser	Arg	Ser	Ala	Asp	Ala	Pro	Ala	Tyr	Gln	Gln	Gly	Gln	Asn	Gln	Leu		
			340					345					350				

Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp  
 355 360 365

Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys  
 370 375 380

Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala  
 385 390 395 400

Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys  
 405 410 415

Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr  
 420 425 430

Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg  
 435 440

<210> 3

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 3

cccaaggcac tgatgttcac cttc

24

<210> 4

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 4

tgagacaaag tccccaatct ctgacag

27

<210> 5

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 5

ctgcagctgc tcctcaagta ctattc

26

<210> 6  
 <211> 28  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 6  
 tccccggagaa ggtccacagt tcctcttt 28

<210> 7  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 7  
 gaagcagcag agggtttgaa gccacatac 29

<210> 8  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 8  
 ggcaggtctt cagttgctta tgaaggt 27

<210> 9  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 9  
 gggtcctctt cagggtccag aatatgt 27

<210> 10  
 <211> 27  
 <212> DNA  
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<220>  
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<400> 10  
gcgaagaact caccctggac tgttcat

27

<210> 11  
<211> 30  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: Primer

<400> 11  
gagctccaca gacaacaaga ggacgcagca

30

<210> 12  
<211> 27  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: Primer

<400> 12  
gagctgacgac gttccttagt gactgtg

27

<210> 13  
<211> 30  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: Primer

<400> 13  
cctcgtcagc ctgttgcca atccttctgg

30

<210> 14  
<211> 28  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: Primer

<400> 14  
cagcctcatc aatctgttct acttggt

28

<210> 15  
<211> 28  
<212> DNA  
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<220>

<223> Description of Artificial Sequence: Primer

<400> 15

ccaccagggg ccacagttta tcattcaa

28

<210> 16

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 16

acctggagag aatcctaagc tcatcat

27

<210> 17

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 17

aggtcttggtg tccctgacag tcctgggt

28

<210> 18

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 18

caagcaaaca ctgtagtgca gagcccttcc

30

<210> 19

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 19

caagacatcc ataactgccc tacag

25

<210> 20

<211> 27



<212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Primer  
  
 <400> 20  
 gtgtatgaaa cccaggacag ttcttac 27  
  
 <210> 21  
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 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Primer  
  
 <400> 21  
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 <210> 22  
 <211> 28  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Primer  
  
 <400> 22  
 caaagctctc catcgctgac tgttcaag 28  
  
 <210> 23  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence  
  
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 <223> Description of Artificial Sequence: Primer  
  
 <400> 23  
 atctaattcct gggaagagca aat 23  
  
 <210> 24  
 <211> 23  
 <212> DNA  
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 <400> 24  
 ggcgtctggt accacgtggt caa 23

<210> 25  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 25  
 gtgaaagggc aaggacaaaa agc 23

<210> 26  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 26  
 gatatgcgaa cagtatctag gc 22

<210> 27  
 <211> 23  
 <212> DNA  
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<220>  
 <223> Description of Artificial Sequence: Primer

<400> 27  
 acataatcaa aggaaagggg gaa 23

<210> 28  
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<220>  
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<400> 28  
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<210> 29  
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<220>  
 <223> Description of Artificial Sequence: Primer

<400> 29  
 tacctgatca aaagaatggg aga 23

<210> 30  
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<220>  
 <223> Description of Artificial Sequence: Primer

<400> 30  
 ataaccatga caatatgtac tgg 23

<210> 31  
 <211> 23  
 <212> DNA  
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<220>  
 <223> Description of Artificial Sequence: Primer

<400> 31  
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<210> 32  
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<220>  
 <223> Description of Artificial Sequence: Primer

<400> 32  
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<210> 33  
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<220>  
 <223> Description of Artificial Sequence: Primer

<400> 33  
 agcttgcaag agttggaaaa cca 23

<210> 34  
 <211> 23  
 <212> DNA  
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<220>  
 <223> Description of Artificial Sequence: Primer  
  
 <400> 34  
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<210> 35  
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 <223> Description of Artificial Sequence: Primer  
  
 <400> 35  
 acaaggtgac agggaaggga caa 23

<210> 36  
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 <212> DNA  
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 <220>  
 <223> Description of Artificial Sequence: Primer  
  
 <400> 36  
 acctacagaa cccaaggact cag 23

<210> 37  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Primer  
  
 <400> 37  
 cagttgccct cggatcgatt ttc 23

<210> 38  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Primer  
  
 <400> 38  
 gccgagatca aggctgtggg cag 23

<210> 39  
 <211> 23

<212> DNA  
 <213> Artificial Sequence  
  
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 <223> Description of Artificial Sequence: Primer  
  
 <400> 39  
 agaaccatct gtaagagtgg aac 23

<210> 40  
 <211> 23  
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 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Primer  
  
 <400> 40  
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<210> 41  
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 <220>  
 <223> Description of Artificial Sequence: Primer  
  
 <400> 41  
 gtagtcctga aaaagggcac act 23

<210> 42  
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 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Primer  
  
 <400> 42  
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<210> 43  
 <211> 393  
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 <213> Homo sapiens  
  
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 <222> (1)..(393)

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 1 5 10 15  
 tgg gtg cag agc cag cag aag gtg cag cag agc cca gaa tcc ctc agt 96  
 Trp Val Gln Ser Gln Gln Lys Val Gln Gln Ser Pro Glu Ser Leu Ser  
 20 25 30  
 gtc cca gag gga ggc atg gcc tct ctc aac tgc act tca agt gat cgc 144  
 Val Pro Glu Gly Gly Met Ala Ser Leu Asn Cys Thr Ser Ser Asp Arg  
 35 40 45  
 aat ttt cag tat ttc tgg tgg tac aga cag cat tct gga gaa ggc ccc 192  
 Asn Phe Gln Tyr Phe Trp Trp Tyr Arg Gln His Ser Gly Glu Gly Pro  
 50 55 60  
 aaa gca ctg atg tcc atc ttc tct gat ggt gac aag aaa gaa ggc aga 240  
 Lys Ala Leu Met Ser Ile Phe Ser Asp Gly Asp Lys Lys Glu Gly Arg  
 65 70 75 80  
 ttc aca gct cac ctc aat aag gcc agc ctg cat gtt tcc ctg cac atc 288  
 Phe Thr Ala His Leu Asn Lys Ala Ser Leu His Val Ser Leu His Ile  
 85 90 95  
 aga gac tcc cag ccc agt gac tcc gct ctc tac ttc tgt gca gtt atg 336  
 Arg Asp Ser Gln Pro Ser Asp Ser Ala Leu Tyr Phe Cys Ala Val Met  
 100 105 110  
 gat tat aac cag ggg aag ctt atc ttt ggg cag ggt acc aag tta tct 384  
 Asp Tyr Asn Gln Gly Lys Leu Ile Phe Gly Gln Gly Thr Lys Leu Ser  
 115 120 125  
 atc aag ccc 393  
 Ile Lys Pro  
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 <210> 44  
 <211> 131  
 <212> PRT  
 <213> Homo sapiens  
 <400> 44  
 Met Lys Ser Leu Ser Val Ser Leu Val Val Leu Trp Leu Gln Leu Asn  
 1 5 10 15  
 Trp Val Gln Ser Gln Gln Lys Val Gln Gln Ser Pro Glu Ser Leu Ser  
 20 25 30  
 Val Pro Glu Gly Gly Met Ala Ser Leu Asn Cys Thr Ser Ser Asp Arg  
 35 40 45  
 Asn Phe Gln Tyr Phe Trp Trp Tyr Arg Gln His Ser Gly Glu Gly Pro  
 50 55 60

Lys Ala Leu Met Ser Ile Phe Ser Asp Gly Asp Lys Lys Glu Gly Arg  
 65 70 75 80  
 Phe Thr Ala His Leu Asn Lys Ala Ser Leu His Val Ser Leu His Ile  
 85 90 95  
 Arg Asp Ser Gln Pro Ser Asp Ser Ala Leu Tyr Phe Cys Ala Val Met  
 100 105 110  
 Asp Tyr Asn Gln Gly Lys Leu Ile Phe Gly Gln Gly Thr Lys Leu Ser  
 115 120 125  
 Ile Lys Pro  
 130

<210> 45  
 <211> 402  
 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> (1)..(402)

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 Met Gly Ser Arg Leu Phe Phe Val Val Ile Leu Leu Cys Ala Lys  
 1 5 10 15  
 cac atg gag gct gca gtc acc caa agt cca aga agc aag gtg gca gta 96  
 His Met Glu Ala Ala Val Thr Gln Ser Pro Arg Ser Lys Val Ala Val  
 20 25 30  
 aca gga gga aag gtg aca ttg agc tgt cac cag act aat aac cat gac 144  
 Thr Gly Gly Lys Val Thr Leu Ser Cys His Gln Thr Asn Asn His Asp  
 35 40 45  
 tat atg tac tgg tat cgg cag gac acg ggg cat ggg ctg agg ctg atc 192  
 Tyr Met Tyr Trp Tyr Arg Gln Asp Thr Gly His Gly Leu Arg Leu Ile  
 50 55 60  
 cat tac tca tat gtc gct gac agc acg gag aaa gga gat atc cct gat 240  
 His Tyr Ser Tyr Val Ala Asp Ser Thr Glu Lys Gly Asp Ile Pro Asp  
 65 70 75 80  
 ggg tac aag gcc tcc aga cca agc caa gag aat ttc tct ctc att ctg 288  
 Gly Tyr Lys Ala Ser Arg Pro Ser Gln Glu Asn Phe Ser Leu Ile Leu  
 85 90 95  
 gag ttg gct tcc ctt tct cag tca gct gta tat ttc tgt gcc agc agc 336  
 Glu Leu Ala Ser Leu Ser Gln Ser Ala Val Tyr Phe Cys Ala Ser Ser  
 100 105 110

gat ttc gcc ggg aca ggg ggc ttc tat gaa cag tac ttc ggt ccc ggc 384  
 Asp Phe Ala Gly Thr Gly Gly Phe Tyr Glu Gln Tyr Phe Gly Pro Gly  
           115                          120                          125

acc agg ctc acg gtt tct 402  
 Thr Arg Leu Thr Val Ser  
           130

<210> 46  
 <211> 134  
 <212> PRT  
 <213> Homo sapiens

<400> 46  
 Met Gly Ser Arg Leu Phe Phe Val Val Leu Ile Leu Leu Cys Ala Lys  
       1                      5                          10                          15  
 His Met Glu Ala Ala Val Thr Gln Ser Pro Arg Ser Lys Val Ala Val  
                       20                          25                          30  
 Thr Gly Gly Lys Val Thr Leu Ser Cys His Gln Thr Asn Asn His Asp  
           35                          40                          45  
 Tyr Met Tyr Trp Tyr Arg Gln Asp Thr Gly His Gly Leu Arg Leu Ile  
       50                          55                          60  
 His Tyr Ser Tyr Val Ala Asp Ser Thr Glu Lys Gly Asp Ile Pro Asp  
       65                          70                          75                          80  
 Gly Tyr Lys Ala Ser Arg Pro Ser Gln Glu Asn Phe Ser Leu Ile Leu  
                       85                          90                          95  
 Glu Leu Ala Ser Leu Ser Gln Ser Ala Val Tyr Phe Cys Ala Ser Ser  
           100                          105                          110  
 Asp Phe Ala Gly Thr Gly Gly Phe Tyr Glu Gln Tyr Phe Gly Pro Gly  
       115                          120                          125  
 Thr Arg Leu Thr Val Ser  
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Lys Leu Val Gly Lys Leu Asn Trp Ala  
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